

0450



OIPE

#2

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/053,510

DATE: 02/07/2002  
 TIME: 12:39:20

Input Set : A:\402c2.app  
 Output Set: N:\CRF3\02072002\J053510.raw

ENTERED

4 <110> APPLICANT: Saba, Julie D.  
 5 Fyrst, Henrik  
 9 <120> TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,  
 10 POLYNUCLEOTIDES AND MODULATING AGENTS AND  
 11 METHODS OF USE THEREFOR  
 13 <130> FILE REFERENCE: 200116.402C2  
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/053,510  
 16 <141> CURRENT FILING DATE: 2002-01-17  
 18 <160> NUMBER OF SEQ ID NOS: 21  
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 1770  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: S. cerevisiae  
 27 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: (1)...(1770)  
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 33 Met Ser Gly Val Ser Asn Lys Thr Val Ser Ile Asn Gly Trp Tyr Gly  
 34 1 5 10 15  
 36 atg cca att cat tta cta agg gaa gaa ggc gac ttt gcc cag ttt atg 96  
 37 Met Pro Ile His Leu Leu Arg Glu Glu Gly Asp Phe Ala Gln Phe Met  
 38 20 25 30  
 40 att cta acc atc aac gaa tta aaa ata gcc ata cat ggt tac ctc aga 144  
 41 Ile Leu Thr Ile Asn Glu Leu Lys Ile Ala Ile His Gly Tyr Leu Arg  
 42 35 40 45  
 44 aat acc cca tgg tac aac atg ttg aag gat tat ttg ttt gtg atc ttt 192  
 45 Asn Thr Pro Trp Tyr Asn Met Leu Lys Asp Tyr Leu Phe Val Ile Phe  
 46 50 55 60  
 48 tgt tac aag cta ata agt aat ttt ttt tat ctg ttg aaa gtt tat ggg 240  
 49 Cys Tyr Lys Leu Ile Ser Asn Phe Phe Tyr Leu Leu Lys Val Tyr Gly  
 50 65 70 75 80  
 52 ccg gtg agg tta gca gtg aga aca tac gag cat agt tcc aga aga ttg 288  
 53 Pro Val Arg Leu Ala Val Arg Thr Tyr Glu His Ser Ser Arg Arg Leu  
 54 85 90 95  
 56 ttt cgt tgg tta ttg gac tca cca ttt ttg agg ggt acc gta gaa aag 336  
 57 Phe Arg Trp Leu Leu Asp Ser Pro Phe Leu Arg Gly Thr Val Glu Lys  
 58 100 105 110  
 60 gaa gtc aca aag gtc aaa caa tcg atc gaa gac gaa cta att aga tcg 384  
 61 Glu Val Thr Lys Val Lys Gln Ser Ile Glu Asp Glu Leu Ile Arg Ser  
 62 115 120 125  
 64 gac tct cag tta atg aat ttc cca cag ttg cca tcc aat ggg ata cct 432

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65 Asp Ser Gln Leu Met Asn Phe Pro Gln Leu Pro Ser Asn Gly Ile Pro
66      130                      135                      140
68 cag gat gat gtt att gaa gag cta aat aaa ttg aac gac ttg ata cca      480
69 Gln Asp Asp Val Ile Glu Glu Leu Asn Lys Leu Asn Asp Leu Ile Pro
70 145                      150                      155                      160
72 cat acc caa tgg aag gaa gga aag gtc tct ggt gcc gtt tac cac ggt      528
73 His Thr Gln Trp Lys Glu Gly Lys Val Ser Gly Ala Val Tyr His Gly
74      165                      170                      175
76 ggt gat gat ttg atc cac tta caa aca atc gca tac gaa aaa tat tgc      576
77 Gly Asp Asp Leu Ile His Leu Gln Thr Ile Ala Tyr Glu Lys Tyr Cys
78      180                      185                      190
80 gtt gcc aat caa tta cat ccc gat gtc ttt cct gcc gta cgt aaa atg      624
81 Val Ala Asn Gln Leu His Pro Asp Val Phe Pro Ala Val Arg Lys Met
82      195                      200                      205
84 gaa tcc gaa gtg gtt tct atg gtt tta aga atg ttt aat gcc cct tct      672
85 Glu Ser Glu Val Val Ser Met Val Leu Arg Met Phe Asn Ala Pro Ser
86      210                      215                      220
88 gat aca ggt tgt ggt acc aca act tca ggt ggt aca gaa tcc ttg ctt      720
89 Asp Thr Gly Cys Gly Thr Thr Thr Ser Gly Gly Thr Glu Ser Leu Leu
90 225                      230                      235                      240
92 tta gca tgt ctg agc gct aaa atg tat gcc ctt cat cat cgt gga atc      768
93 Leu Ala Cys Leu Ser Ala Lys Met Tyr Ala Leu His His Arg Gly Ile
94      245                      250                      255
96 acc gaa cca gaa ata att gct ccc gta act gca cat gct ggg ttt gac      816
97 Thr Glu Pro Glu Ile Ile Ala Pro Val Thr Ala His Ala Gly Phe Asp
98      260                      265                      270
100 aaa gct gct tat tac ttt ggc atg aag cta cgc cac gtg gag cta gat      864
101 Lys Ala Ala Tyr Tyr Phe Gly Met Lys Leu Arg His Val Glu Leu Asp
102      275                      280                      285
104 cca acg aca tat caa gtg gac ctg gga aaa gtg aaa aaa ttc atc aat      912
105 Pro Thr Thr Tyr Gln Val Asp Leu Gly Lys Val Lys Lys Phe Ile Asn
106      290                      295                      300
108 aag aac aca att tta ctg gtc ggt tcc gct cca aac ttt cct cat ggt      960
109 Lys Asn Thr Ile Leu Leu Val Gly Ser Ala Pro Asn Phe Pro His Gly
110 305                      310                      315                      320
112 att gcc gat gat att gaa gga ttg ggt aaa ata gca caa aaa tat aaa      1008
113 Ile Ala Asp Asp Ile Glu Gly Leu Gly Lys Ile Ala Gln Lys Tyr Lys
114      325                      330                      335
116 ctt cct tta cac gtc gac agt tgt cta ggt tcc ttt att gtt tca ttt      1056
117 Leu Pro Leu His Val Asp Ser Cys Leu Gly Ser Phe Ile Val Ser Phe
118      340                      345                      350
120 atg gaa aag gct ggt tac aaa aat ctg cca tta ctt gac ttt aga gtc      1104
121 Met Glu Lys Ala Gly Tyr Lys Asn Leu Pro Leu Leu Asp Phe Arg Val
122      355                      360                      365
124 ccg gga gtc acc tca ata tca tgt gac act cat aaa tat gga ttt gca      1152
125 Pro Gly Val Thr Ser Ile Ser Cys Asp Thr His Lys Tyr Gly Phe Ala
126      370                      375                      380
128 cca aaa ggc tcg tca gtt ata atg tat aga aac agc gac tta cga atg      1200
129 Pro Lys Gly Ser Ser Val Ile Met Tyr Arg Asn Ser Asp Leu Arg Met

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130 385          390          395          400
132 cat cag tat tac gta aat cct gct tgg act ggc ggg tta tat ggc tct 1248
133 His Gln Tyr Tyr Val Asn Pro Ala Trp Thr Gly Gly Leu Tyr Gly Ser
134          405          410          415
136 cct aca tta gca ggg tcc agg cct ggt gct att gtc gta ggt tgt tgg 1296
137 Pro Thr Leu Ala Gly Ser Arg Pro Gly Ala Ile Val Val Gly Cys Trp
138          420          425          430
140 gcc act atg gtc aac atg ggt gaa aat ggg tac att gag tcg tgc caa 1344
141 Ala Thr Met Val Asn Met Gly Glu Asn Gly Tyr Ile Glu Ser Cys Gln
142          435          440          445
144 gaa ata gtc ggt gca gca atg aag ttt aaa aaa tac atc cag gaa aac 1392
145 Glu Ile Val Gly Ala Ala Met Lys Phe Lys Lys Tyr Ile Gln Glu Asn
146          450          455          460
148 att cca gac ctg aat ata atg ggc aac cct aga tat tca gtc att tca 1440
149 Ile Pro Asp Leu Asn Ile Met Gly Asn Pro Arg Tyr Ser Val Ile Ser
150 465          470          475          480
152 ttt tct tca aag acc ttg aac ata cac gaa cta tct gac agg ttg tcc 1488
153 Phe Ser Ser Lys Thr Leu Asn Ile His Glu Leu Ser Asp Arg Leu Ser
154          485          490          495
156 aag aaa ggc tgg cat ttc aat gcc cta caa aag ccg gtt gca cta cac 1536
157 Lys Lys Gly Trp His Phe Asn Ala Leu Gln Lys Pro Val Ala Leu His
158          500          505          510
160 atg gcc ttc acg aga ttg agc gct cat gtt gtg gat gag atc tgc gac 1584
161 Met Ala Phe Thr Arg Leu Ser Ala His Val Val Asp Glu Ile Cys Asp
162          515          520          525
164 att tta cgt act acc gtg caa gag ttg aag agc gaa tca aat tct aaa 1632
165 Ile Leu Arg Thr Thr Val Gln Glu Leu Lys Ser Glu Ser Asn Ser Lys
166          530          535          540
168 cca tcc cca gac gga act agc gct cta tat ggt gtc gcc ggg agc gtt 1680
169 Pro Ser Pro Asp Gly Thr Ser Ala Leu Tyr Gly Val Ala Gly Ser Val
170 545          550          555          560
172 aaa act gct ggc gtt gca gac aaa ttg att gtg gga ttc cta gac gca 1728
173 Lys Thr Ala Gly Val Ala Asp Lys Leu Ile Val Gly Phe Leu Asp Ala
174          565          570          575
176 tta tac aag ttg ggt cca gga gag gat acc gcc acc aag tag 1770
177 Leu Tyr Lys Leu Gly Pro Gly Glu Asp Thr Ala Thr Lys *
178          580          585
182 <210> SEQ ID NO: 2
183 <211> LENGTH: 589
184 <212> TYPE: PRT
185 <213> ORGANISM: S. cerevisiae
187 <400> SEQUENCE: 2
188 Met Ser Gly Val Ser Asn Lys Thr Val Ser Ile Asn Gly Trp Tyr Gly
189 1          5          10          15
190 Met Pro Ile His Leu Leu Arg Glu Glu Gly Asp Phe Ala Gln Phe Met
191          20          25          30
192 Ile Leu Thr Ile Asn Glu Leu Lys Ile Ala Ile His Gly Tyr Leu Arg
193          35          40          45
194 Asn Thr Pro Trp Tyr Asn Met Leu Lys Asp Tyr Leu Phe Val Ile Phe

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195	50	55	60
196	Cys Tyr Lys Leu Ile Ser Asn Phe Phe Tyr Leu Leu Lys Val Tyr Gly		
197	65	70	75
198	Pro Val Arg Leu Ala Val Arg Thr Tyr Glu His Ser Ser Arg Arg Leu		
199		85	90
200	Phe Arg Trp Leu Leu Asp Ser Pro Phe Leu Arg Gly Thr Val Glu Lys		
201		100	105
202	Glu Val Thr Lys Val Lys Gln Ser Ile Glu Asp Glu Leu Ile Arg Ser		
203		115	120
204	Asp Ser Gln Leu Met Asn Phe Pro Gln Leu Pro Ser Asn Gly Ile Pro		
205		130	135
206	Gln Asp Asp Val Ile Glu Leu Asn Lys Leu Asn Asp Leu Ile Pro		
207	145	150	155
208	His Thr Gln Trp Lys Glu Gly Lys Val Ser Gly Ala Val Tyr His Gly		
209		165	170
210	Gly Asp Asp Leu Ile His Leu Gln Thr Ile Ala Tyr Glu Lys Tyr Cys		
211		180	185
212	Val Ala Asn Gln Leu His Pro Asp Val Phe Pro Ala Val Arg Lys Met		
213		195	200
214	Glu Ser Glu Val Val Ser Met Val Leu Arg Met Phe Asn Ala Pro Ser		
215		210	215
216	Asp Thr Gly Cys Gly Thr Thr Thr Ser Gly Gly Thr Glu Ser Leu Leu		
217	225	230	235
218	Leu Ala Cys Leu Ser Ala Lys Met Tyr Ala Leu His His Arg Gly Ile		
219		245	250
220	Thr Glu Pro Glu Ile Ile Ala Pro Val Thr Ala His Ala Gly Phe Asp		
221		260	265
222	Lys Ala Ala Tyr Tyr Phe Gly Met Lys Leu Arg His Val Glu Leu Asp		
223		275	280
224	Pro Thr Thr Tyr Gln Val Asp Leu Gly Lys Val Lys Lys Phe Ile Asn		
225		290	295
226	Lys Asn Thr Ile Leu Leu Val Gly Ser Ala Pro Asn Phe Pro His Gly		
227	305	310	315
228	Ile Ala Asp Asp Ile Glu Gly Leu Gly Lys Ile Ala Gln Lys Tyr Lys		
229		325	330
230	Leu Pro Leu His Val Asp Ser Cys Leu Gly Ser Phe Ile Val Ser Phe		
231		340	345
232	Met Glu Lys Ala Gly Tyr Lys Asn Leu Pro Leu Leu Asp Phe Arg Val		
233		355	360
234	Pro Gly Val Thr Ser Ile Ser Cys Asp Thr His Lys Tyr Gly Phe Ala		
235		370	375
236	Pro Lys Gly Ser Ser Val Ile Met Tyr Arg Asn Ser Asp Leu Arg Met		
237	385	390	395
238	His Gln Tyr Tyr Val Asn Pro Ala Trp Thr Gly Gly Leu Tyr Gly Ser		
239		405	410
240	Pro Thr Leu Ala Gly Ser Arg Pro Gly Ala Ile Val Val Gly Cys Trp		
241		420	425
242	Ala Thr Met Val Asn Met Gly Glu Asn Gly Tyr Ile Glu Ser Cys Gln		
243		435	440
			445

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Input Set : A:\402c2.app

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244 Glu Ile Val Gly Ala Ala Met Lys Phe Lys Lys Tyr Ile Gln Glu Asn
245      450      455      460
246 Ile Pro Asp Leu Asn Ile Met Gly Asn Pro Arg Tyr Ser Val Ile Ser
247 465      470      475      480
248 Phe Ser Ser Lys Thr Leu Asn Ile His Glu Leu Ser Asp Arg Leu Ser
249      485      490      495
250 Lys Lys Gly Trp His Phe Asn Ala Leu Gln Lys Pro Val Ala Leu His
251      500      505      510
252 Met Ala Phe Thr Arg Leu Ser Ala His Val Val Asp Glu Ile Cys Asp
253      515      520      525
254 Ile Leu Arg Thr Thr Val Gln Glu Leu Lys Ser Glu Ser Asn Ser Lys
255      530      535      540
256 Pro Ser Pro Asp Gly Thr Ser Ala Leu Tyr Gly Val Ala Gly Ser Val
257 545      550      555      560
258 Lys Thr Ala Gly Val Ala Asp Lys Leu Ile Val Gly Phe Leu Asp Ala
259      565      570      575
260 Leu Tyr Lys Leu Gly Pro Gly Glu Asp Thr Ala Thr Lys
261      580      585
264 <210> SEQ ID NO: 3
265 <211> LENGTH: 1629
266 <212> TYPE: DNA
267 <213> ORGANISM: C. elegans
269 <220> FEATURE:
270 <221> NAME/KEY: CDS
271 <222> LOCATION: (1)...(1629)
273 <400> SEQUENCE: 3
274 atg gat ttt gca ctg gag caa tat cat agt gca aag gat ttg tta ata 48
275 Met Asp Phe Ala Leu Glu Gln Tyr His Ser Ala Lys Asp Leu Leu Ile
276 1      5      10      15
278 ttt gag ctt cga aag ttc aat cca att gtt ctg gtt tct agt act att 96
279 Phe Glu Leu Arg Lys Phe Asn Pro Ile Val Leu Val Ser Ser Thr Ile
280      20      25      30
282 gtt gca aca tac gta ctc acc aat ctg aga cat atg cat tta gat gaa 144
283 Val Ala Thr Tyr Val Leu Thr Asn Leu Arg His Met His Leu Asp Glu
284      35      40      45
286 atg ggc atc cgg aaa cgt ttg agc act tgg ttt ttc acc act gta aag 192
287 Met Gly Ile Arg Lys Arg Leu Ser Thr Trp Phe Phe Thr Thr Val Lys
288      50      55      60
290 cgt gtg cct ttc atc agg aaa atg att gac aaa caa cta aac gaa gta 240
291 Arg Val Pro Phe Ile Arg Lys Met Ile Asp Lys Gln Leu Asn Glu Val
292 65      70      75      80
294 aag gac gag ctt gag aaa agt ctg aga att gtg gat cga agc acc gaa 288
295 Lys Asp Glu Leu Glu Lys Ser Leu Arg Ile Val Asp Arg Ser Thr Glu
296      85      90      95
298 tac ttc act aca atc cca agc cat tca gtt gga aga act gaa gta ctt 336
299 Tyr Phe Thr Thr Ile Pro Ser His Ser Val Gly Arg Thr Glu Val Leu
300      100      105      110
302 cgc ctt gct gcc atc tat gat gat ttg gaa gga cca gct ttt ttg gaa 384
303 Arg Leu Ala Ala Ile Tyr Asp Asp Leu Glu Gly Pro Ala Phe Leu Glu

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VERIFICATION SUMMARY

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DATE: 02/07/2002

TIME: 12:39:21

Input Set : A:\402c2.app

Output Set: N:\CRF3\02072002\J053510.raw

L:15 M:270 C: Current Application Number differs, Wrong Format